

SEQUENCE LISTING

<110> Kretz, Keith

<120> NOVEL PHYTASE

<130> 09010/029003

<140> 09/291,931

<141> 1999-04-13

<150> 08/910,798

<151> 1997-08-13

<150> 09/259,214

<151> 1999-03-01

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1323

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1320)

<221> misc_feature

<222> (1)...(1323)

<223> n = A,T,C or G

<400> 1

atg	aaa	gcg	atc	tta	atc	cca	ttt	tta	tct	ctt	ctg	att	ccg	tta	acc	48
Met	Lys	Ala	Ile	Leu	Ile	Pro	Phe	Leu	Ser	Leu	Leu	Ile	Pro	Leu	Thr	
1				5					10					15		

ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			

gtg	gtg	att	gtc	agt	cgt	cat	ggg	gtg	cgt	gct	cca	acc	aag	gcc	acg	144
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
		35					40					45				

caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	192
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
	50					55					60					

aaa	ctg	ggg	tgg	ctg	aca	ccg	cg	ggg	ggg	gag	cta	atc	gcc	tat	ctc	240
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	
	65				70				75						80	

gga	cat	tac	caa	cgc	cag	cgt	ctg	gta	gcc	gac	gga	ttg	ctg	gcg	aaa	288
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
			85					90							95	



T, 0350

B1

35

aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp 100 105 110	336
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro 115 120 125	384
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp 130 135 140	432
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala 145 150 155 160	480
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp 165 170 175	528
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu 180 185 190	576
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu 195 200 205	624
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala 210 215 220	672
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr 225 230 235 240	720
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp 245 250 255	768
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His 260 265 270	816
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285	864
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His 290 295 300	912
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305 310 315 320	960
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu 325 330 335	1008

gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 350	
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385 390 395 400	
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405 410 415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
420 425 430	
aga tct cat cac cat cac cat cac taa	1323
Arg Ser His His His His His His	
435 440	

<210> 2

<211> 440

<212> PRT

<213> Escherichia coli

<400> 2

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
1 5 10 15	
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	

Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
 210 215 220
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430
 Arg Ser His His His His His
 435 440

<210> 3
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 3
 gtttctgaat tcaaggagga atttaaataa aagcgatctt aatcccatt

49

<210> 4
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 4
 gtttctggat ccttacaac tgcacgccgg tat

33